

P. Ruffey

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/727,084

TECH CENTER 1600/2900

DATE: 10/30/98
TIME: 09:44:55

INPUT SET: S29524.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

p#31

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SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Pulst, Stefan M
6
7 (ii) TITLE OF INVENTION: NUCLEIC ACID ENCODING SPINOCEREBELLAR
8 ATAXIA-2 AND PRODUCTS RELATED THERETO
9
10 (iii) NUMBER OF SEQUENCES: 19
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: Muetting, Raasch & Gebhardt, P.A.
14 (B) STREET: 119 North Fourth Street
15 (C) CITY: Minneapolis
16 (D) STATE: Minnesota
17 (E) COUNTRY: USA
18 (F) ZIP: 55401
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER: US 08/727,084
28 (B) FILING DATE: 08-OCT-1996
29 (C) CLASSIFICATION:
30
31 (viii) ATTORNEY/AGENT INFORMATION:
32 (A) NAME: Muetting, Ann M.
33 (B) REGISTRATION NUMBER: 33,977
34 (C) REFERENCE/DOCKET NUMBER: 232.00010101
35
36 (ix) TELECOMMUNICATION INFORMATION:
37 (A) TELEPHONE: 612/305-1220
38 (B) TELEFAX: 612/305-1228
39
40
41
42 (2) INFORMATION FOR SEQ ID NO:1:
43
44 (i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 516 base pairs
46 (B) TYPE: nucleic acid

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47          (C) STRANDEDNESS: both
48          (D) TOPOLOGY: both
49
50      (ii) MOLECULE TYPE: DNA (genomic)
51
52
53
54      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
55
56      TTGGTAGCAA CGGAAACGGC GGCGGCGCGT TTCGGCCCCG CTCCCGGCGG CTCCTTGGTC      60
57
58      TCGGCGGGCC TCCCCGCCCC TTCGTCTGTC TCCTTCTCCC CCTCGCCAGC CCGGGCGCCC      120
59
60      CTCCGGCCGC GCCAACCCGC GCCTCCCCGC TCGGCGCCCC TGCGTCCCCG CCGCGTTCCG      180
61
62      GCGTCTCCTT GGCGCGCCCC GCTCCCGGCT GTCCCCGCCC GGCGTGCGAG CCGGTGTATG      240
63
64      GGCCCCTCAC CATGTCGCTG AAGCCCCAGC AGCAGCAGCA GCAGCAGCAG CAACAGCAGC      300
65
66      AGCAGCAACA GCAGCAGCAG CAGCAGCAGC AGCCGCCGCC CGCGGCTGCC AATGTCCGCA      360
67
68      AGCCCGGCGG CAGCGGCCTT CTAGCGTCGC CCGCCGCCGC GCCTTCGCCG TCCTCGTCTT      420
69
70      CGGTCTCCTC GTCCTCGGCC ACGGCTCCCT CCTCGGTGGT CGCGGCGACC TCCGGCGGCG      480
71
72      GGAGGCCCCG CCTGGGCAGG TGGGTGTCGG CACCCC      516
73
74      (2) INFORMATION FOR SEQ ID NO:2:
75
76      (i) SEQUENCE CHARACTERISTICS:
77          (A) LENGTH: 4481 base pairs
78          (B) TYPE: nucleic acid
79          (C) STRANDEDNESS: both
80          (D) TOPOLOGY: both
81
82      (ii) MOLECULE TYPE: cDNA
83
84
85      (ix) FEATURE:
86          (A) NAME/KEY: CDS
87          (B) LOCATION: 163..4101
88
89
90      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
91
92      ACCCCCGAGA AAGCAACCCA GCGCGCCGCC CGCTCCTCAC GTGTCCCTCC CGGCCCCGGG      60
93
94      GCCACCTCAC GTTCTGCTTC CGTCTGACCC CTCCGACTTC CGGTAAAGAG TCCCTATCCG      120
95
96      CACCTCCGCT CCCACCCGGC GCCTCGGCGC GCCCGCCCTC CG ATG CGC TCA GCG      174
97          Met Arg Ser Ala
98
99

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100	GCC GCA GCT CCT CGG AGT CCC GCG GTG GCC ACC GAG TCT CGC CGC TTC	222
101	Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu Ser Arg Arg Phe	
102	5 10 15 20	
103		
104	GCC GCA GCC AGG TGG CCC GGG TGG CGC TCG CTC CAG CGG CCG GCG CGG	270
105	Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln Arg Pro Ala Arg	
106	25 30 35	
107		
108	CGG AGC GGG CGG GGC GGC GGT GGC GCG GCC CCG GGA CCG TAT CCC TCC	318
109	Arg Ser Gly Arg Gly Gly Gly Gly Ala Ala Pro Gly Pro Tyr Pro Ser	
110	40 45 50	
111		
112	GCC GCC CCT CCC CCG CCC GGC CCC GGC CCC CCT CCC TCC CGG CAG AGC	366
113	Ala Ala Pro Pro Pro Pro Gly Pro Gly Pro Pro Pro Ser Arg Gln Ser	
114	55 60 65	
115		
116	TCG CCT CCC TCC GCC TCA GAC TGT TTT GGT AGC AAC GGC AAC GGC GGC	414
117	Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn Gly Asn Gly Gly	
118	70 75 80	
119		
120	GGC GCG TTT CGG CCC GGC TCC CGG CGG CTC CTT GGT CTC GGC GGG CCT	462
121	Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Leu Gly Leu Gly Gly Pro	
122	85 90 95 100	
123		
124	CCC CGC CCC TTC GTC GTC GTC CTT CTC CCC CTC GCC AGC CCG GGC GCC	510
125	Pro Arg Pro Phe Val Val Val Leu Leu Pro Leu Ala Ser Pro Gly Ala	
126	105 110 115	
127		
128	CCT CCG GCC GCG CCA ACC CGC GCC TCC CCG CTC GGC GCC CGT GCG TCC	558
129	Pro Pro Ala Ala Pro Thr Arg Ala Ser Pro Leu Gly Ala Arg Ala Ser	
130	120 125 130	
131		
132	CCG CCG CGT TCC GGC GTC TCC TTG GCG CGC CCG GCT CCC GGC TGT CCC	606
133	Pro Pro Arg Ser Gly Val Ser Leu Ala Arg Pro Ala Pro Gly Cys Pro	
134	135 140 145	
135		
136	CGC CCG GCG TGC GAG CCG GTG TAT GGG CCC CTC ACC ATG TCG CTG AAG	654
137	Arg Pro Ala Cys Glu Pro Val Tyr Gly Pro Leu Thr Met Ser Leu Lys	
138	150 155 160	
139		
140	CCC CAG CAG CAG CAG CAG CAG CAG CAG CAA CAG CAG CAG CAG CAA CAG	702
141	Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln	
142	165 170 175 180	
143		
144	CAG CAG CAG CAG CAG CAG CAG CCG CCG CCC GCG GCT GCC AAT GTC CGC	750
145	Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro Ala Ala Ala Asn Val Arg	
146	185 190 195	
147		
148	AAG CCC GGC GGC AGC GGC CTT CTA GCG TCG CCC GCC GCC GCG CCT TCG	798
149	Lys Pro Gly Gly Ser Gly Leu Leu Ala Ser Pro Ala Ala Ala Pro Ser	
150	200 205 210	
151		
152	CCG TCC TCG TCC TCG GTC TCC TCG TCC TCG GCC ACG GCT CCC TCC TCG	846

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153	Pro	Ser	Ser	Ser	Ser	Val	Ser	Ser	Ser	Ser	Ala	Thr	Ala	Pro	Ser	Ser	
154			215					220					225				
155																	
156	GTG	GTC	GCG	GCG	ACC	TCC	GGC	GGC	GGG	AGG	CCC	GGC	CTG	GGC	AGA	GGT	894
157	Val	Val	Ala	Ala	Thr	Ser	Gly	Gly	Gly	Arg	Pro	Gly	Leu	Gly	Arg	Gly	
158		230					235					240					
159																	
160	CGA	AAC	AGT	AAC	AAA	GGA	CTG	CCT	CAG	TCT	ACG	ATT	TCT	TTT	GAT	GGA	942
161	Arg	Asn	Ser	Asn	Lys	Gly	Leu	Pro	Gln	Ser	Thr	Ile	Ser	Phe	Asp	Gly	
162	245					250					255				260		
163																	
164	ATC	TAT	GCA	AAT	ATG	AGG	ATG	GTT	CAT	ATA	CTT	ACA	TCA	GTT	GTT	GGC	990
165	Ile	Tyr	Ala	Asn	Met	Arg	Met	Val	His	Ile	Leu	Thr	Ser	Val	Val	Gly	
166				265					270						275		
167																	
168	TCC	AAA	TGT	GAA	GTA	CAA	GTG	AAA	AAT	GGA	GGT	ATA	TAT	GAA	GGA	GTT	1038
169	Ser	Lys	Cys	Glu	Val	Gln	Val	Lys	Asn	Gly	Gly	Ile	Tyr	Glu	Gly	Val	
170				280					285				290				
171																	
172	TTT	AAA	ACT	TAC	AGT	CCG	AAG	TGT	GAT	TTG	GTA	CTT	GAT	GCC	GCA	CAT	1086
173	Phe	Lys	Thr	Tyr	Ser	Pro	Lys	Cys	Asp	Leu	Val	Leu	Asp	Ala	Ala	His	
174			295					300					305				
175																	
176	GAG	AAA	AGT	ACA	GAA	TCC	AGT	TCG	GGG	CCG	AAA	CGT	GAA	GAA	ATA	ATG	1134
177	Glu	Lys	Ser	Thr	Glu	Ser	Ser	Ser	Gly	Pro	Lys	Arg	Glu	Glu	Ile	Met	
178		310					315					320					
179																	
180	GAG	AGT	ATT	TTG	TTC	AAA	TGT	TCA	GAC	TTT	GTT	GTG	GTA	CAG	TTT	AAA	1182
181	Glu	Ser	Ile	Leu	Phe	Lys	Cys	Ser	Asp	Phe	Val	Val	Val	Gln	Phe	Lys	
182	325					330				335					340		
183																	
184	GAT	ATG	GAC	TCC	AGT	TAT	GCA	AAA	AGA	GAT	GCT	TTT	ACT	GAC	TCT	GCT	1230
185	Asp	Met	Asp	Ser	Ser	Tyr	Ala	Lys	Arg	Asp	Ala	Phe	Thr	Asp	Ser	Ala	
186				345						350					355		
187																	
188	ATC	AGT	GCT	AAA	GTG	AAT	GGC	GAA	CAC	AAA	GAG	AAG	GAC	CTG	GAG	CCC	1278
189	Ile	Ser	Ala	Lys	Val	Asn	Gly	Glu	His	Lys	Glu	Lys	Asp	Leu	Glu	Pro	
190			360					365					370				
191																	
192	TGG	GAT	GCA	GGT	GAA	CTC	ACA	GCC	AAT	GAG	GAA	CTT	GAG	GCT	TTG	GAA	1326
193	Trp	Asp	Ala	Gly	Glu	Leu	Thr	Ala	Asn	Glu	Glu	Leu	Glu	Ala	Leu	Glu	
194			375					380					385				
195																	
196	AAT	GAC	GTA	TCT	AAT	GGA	TGG	GAT	CCC	AAT	GAT	ATG	TTT	CGA	TAT	AAT	1374
197	Asn	Asp	Val	Ser	Asn	Gly	Trp	Asp	Pro	Asn	Asp	Met	Phe	Arg	Tyr	Asn	
198		390					395					400					
199																	
200	GAA	GAA	AAT	TAT	GGT	GTA	GTG	TCT	ACG	TAT	GAT	AGC	AGT	TTA	TCT	TCG	1422
201	Glu	Glu	Asn	Tyr	Gly	Val	Val	Ser	Thr	Tyr	Asp	Ser	Ser	Leu	Ser	Ser	
202	405					410				415					420		
203																	
204	TAT	ACA	GTG	CCC	TTA	GAA	AGA	GAT	AAC	TCA	GAA	GAA	TTT	TTA	AAA	CGG	1470
205	Tyr	Thr	Val	Pro	Leu	Glu	Arg	Asp	Asn	Ser	Glu	Glu	Phe	Leu	Lys	Arg	

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206	425							430							435							
207																						
208	GAA	GCA	AGG	GCA	AAC	CAG	TTA	GCA	GAA	GAA	ATT	GAG	TCA	AGT	GCC	CAG		1518				
209	Glu	Ala	Arg	Ala	Asn	Gln	Leu	Ala	Glu	Glu	Ile	Glu	Ser	Ser	Ala	Gln						
210				440					445					450								
211																						
212	TAC	AAA	GCT	CGA	GTG	GCC	CTG	GAA	AAT	GAT	GAT	AGG	AGT	GAG	GAA	GAA		1566				
213	Tyr	Lys	Ala	Arg	Val	Ala	Leu	Glu	Asn	Asp	Asp	Arg	Ser	Glu	Glu	Glu						
214			455					460					465									
215																						
216	AAA	TAC	ACA	GCA	GTT	CAG	AGA	AAT	TCC	AGT	GAA	CGT	GAG	GGG	CAC	AGC		1614				
217	Lys	Tyr	Thr	Ala	Val	Gln	Arg	Asn	Ser	Ser	Glu	Arg	Glu	Gly	His	Ser						
218		470					475					480										
219																						
220	ATA	AAC	ACT	AGG	GAA	AAT	AAA	TAT	ATT	CCT	CCT	GGA	CAA	AGA	AAT	AGA		1662				
221	Ile	Asn	Thr	Arg	Glu	Asn	Lys	Tyr	Ile	Pro	Pro	Gly	Gln	Arg	Asn	Arg						
222	485					490					495					500						
223																						
224	GAA	GTC	ATA	TCC	TGG	GGA	AGT	GGG	AGA	CAG	AAT	TCA	CCG	CGT	ATG	GGC		1710				
225	Glu	Val	Ile	Ser	Trp	Gly	Ser	Gly	Arg	Gln	Asn	Ser	Pro	Arg	Met	Gly						
226					505					510					515							
227																						
228	CAG	CCT	GGA	TCG	GGC	TCC	ATG	CCA	TCA	AGA	TCC	ACT	TCT	CAC	ACT	TCA		1758				
229	Gln	Pro	Gly	Ser	Gly	Ser	Met	Pro	Ser	Arg	Ser	Thr	Ser	His	Thr	Ser						
230				520					525					530								
231																						
232	GAT	TTC	AAC	CCG	AAT	TCT	GGT	TCA	GAC	CAA	AGA	GTA	GTT	AAT	GGA	GGT		1806				
233	Asp	Phe	Asn	Pro	Asn	Ser	Gly	Ser	Asp	Gln	Arg	Val	Val	Asn	Gly	Gly						
234			535					540					545									
235																						
236	GTT	CCC	TGG	CCA	TCG	CCT	TGC	CCA	TCT	CCT	TCC	TCT	CGC	CCA	CCT	TCT		1854				
237	Val	Pro	Trp	Pro	Ser	Pro	Cys	Pro	Ser	Pro	Ser	Ser	Arg	Pro	Pro	Ser						
238		550					555						560									
239																						
240	CGC	TAC	CAG	TCA	GGT	CCC	AAC	TCT	CTT	CCA	CCT	CGG	GCA	GCC	ACC	CCT		1902				
241	Arg	Tyr	Gln	Ser	Gly	Pro	Asn	Ser	Leu	Pro	Pro	Arg	Ala	Ala	Thr	Pro						
242	565					570					575					580						
243																						
244	ACA	CGG	CCG	CCC	TCC	AGG	CCC	CCC	TCG	CGG	CCA	TCC	AGA	CCC	CCG	TCT		1950				
245																						

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